

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Herrmann, Stephen H.  
Lu, Zhijian  
McCoy, John M.  
Swanberg, Stephen L.  
Walker, Bruce  
Yang, Otto

(ii) TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
1 5 10 15

Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
20 25 30

Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
35 40 45

Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
50 55 60

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
65 70 75 80

Glu Tyr Leu Glu Lys Ala Leu Asn Lys  
85

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
1 5 10 15

Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
20 25 30

Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
35 40 45

Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
50 55 60

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
65 70 75 80

Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
85 90

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1856 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTCCGTCAG CCGCATTGCC CGCTCGGCGT CCGGCCCCCG ACCCGTGCTC GTCCGCCCGC	60
CCGCCCGCCC GCCCGCGCCA TGAACGCCAA GGTCGTGGTC GTGCTGGTCC TCGTGCTGAC	120
CGCGCTCTGC CTCAGCGACG GGAAGCCCGT CAGCCTGAGC TACAGATGCC CATGCCGATT	180
CTTCGAAAGC CATGTTGCCA GAGCCAACGT CAAGCATCTC AAAATTCTCA ACACTCCAAA	240
CTGTGCCCTT CAGATTGTAG CCCGGCTGAA GAACAACAAC AGACAAGTGT GCATTGACCC	300
GAAGCTAAAG TGGATTCAAG AGTACCTGGA GAAAGCTTTA AACAAAGTAAG CACAACAGCC	360
AAAAAGGACT TTCCGCTAGA CCCACTCGAG GAAAACTAAA ACCTTGTGAG AGATGAAAGG	420
GCAAAGACGT GGGGGAGGGG GCCTTAACCA TGAGGACCAG GTGTGTGTGT GGGGTGGGCA	480
CATTGATCTG GGATCGGGCC TGAGGTTTGC AGCATTAGA CCCTGCATTT ATAGCATAACG	540
GTATGATATT GCAGCTTATA TTCATCCATG CCCTGTACCT GTGCACGTTG GAACTTTAT	600
TACTGGGTT TTTCTTAGAA AGAAATTGTA TTATCAACAG CATTTCAG CAGTTAGTTC	660
CTTCATGATC ATCACAAATCA TCATCATTCT CATTCTCATT TTTAAATCA ACGAGTACTT	720
CAAGATCTGA ATTTGGCTTG TTTGGAGCAT CTCCTCTGCT CCCCTGGGA GTCTGGCAC	780
AGTCAGGTGG TGGCTTAACA GGGAGCTGGA AAAAGTGTCC TTTCTTCAGA CACTGAGGCT	840
CCCGCAGCAG CGCCCCCTCCC AAGAGGAAGG CCTCTGTGGC ACTCAGATAC CGACTGGGC	900
TGGGGCGCCG CCACTGCCTT CACCTCCTCT TTCAAACCTC AGTGATTGGC TCTGTGGCT	960
CCATGTAGAA GCCACTATTA CTGGGACTGT CTCAGAGACC CCTCTCCCAG CTATTCCATC	1020
TCTCTCCCCG ACTCCGAGAG CATGCTTAAT CTTGCTTCTG CTTCTCATT CTGTAGCCTG	1080
ATCAGCGCCG CACCAGCCGG GAAGAGGGTG ATTGCTGGGG CTCGTGCCCT GCATCCCTCT	1140
CCTCCCCAGGG CCTGCCAAC AGCTCGGGCC CTCTGTGAGA TCCGTCTTTG GCCTCCTCCA	1200

GAATGGAGCT GGCCCTCTCC TGGGGATGTG TAATGGTCCC CCTGCTTACC CGCAAAAGAC	1260
AAGTCTTAC AGAATCAAAT GCAATTAA ATCTGAGAGC TCGCTTGAGT GACTGGTTT	1320
GTGATTGCCT CTGAAGCCTA TGTATGCCAT GGAGGCACTA ACAAACTCTG AGGTTTCCGA	1380
AATCAGAAGC GAAAAAAATCA GTGAATAAAC CATCATCTTGC CCACTACCCCC CTCCTGAAGC	1440
CACAGCAGGG GTTCAGGTTC CAATCAGAAC TGTTGGCAAG GTGACATTTC CATGCATAGA	1500
TGCGATCCAC AGAAGGTCCCT GGTGGTATTT GTAACCTTTT GCAAGGCATT TTTTTATATA	1560
TATTTTGTTG CACATTTTTT TTTACGATTC TTTAGAAAAC AAATGTATTT CAAAATATAT	1620
TTATAGTCGA ACAAGTCATA TATATGAATG AGAGCCATAT GAATGTCAGT AGTTTATACT	1680
TCTCTATTAT CTCAAACTAC TGGCAATTG TAAAGAAATA TATATGATAT ATAAATGTGA	1740
TTGCAGCTTT TCAATGTTAG CCACAGTGTA TTTTTTCACT TGTACTAAAA TTGTATCAA	1800
TGTGACATTA TATGCACTAG CAATAAAATG CTAATTGTTT CATGGTAAAA AAAAAA	1856

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3526 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTCCGTCAG CCGCATTGCC CGCTCGGCGT CCGGCCCCCG ACCCGTGCTC GTCCGCCCGC	60
CCGCCCGCCC GCCCGCGCCA TGAACGCCAA GGTCGTGGTC GTGCTGGTCC TCGTGTGAC	120
CGCGCTCTGC CTCAGCGACG GGAAGCCCGT CAGCCTGAGC TACAGATGCC CATGCCGATT	180
CTTCGAAAGC CATGTTGCCA GAGCCAACGT CAAGCATCTC AAAATTCTCA ACACCTCCAAA	240
CTGTGCCCTT CAGATTGTAG CCCGGCTGAA GAACAACAAC AGACAAGTGT GCATTGACCC	300
GAAGCTAAAG TGGATTCAAG AGTACCTGGA GAAAGCTTTA AACAAAGAGGT TCAAGATGTG	360
AGAGGGTCAC ACGCCTGAGG AACCCCTTACA GTAGGAGCCC AGCTCTGAAA CCAGTGTAG	420
GGAAGGGCCT GCCACAGCCT CCCCTGCCAG GGCAGGCCCG CAGGCATTGC CAAGGGCTTT	480
GTTCAGGACCA CTTTGCCATA TTTTCACCAT TTGATTATGT AGCAAAATAC ATGACATTAA	540

TTTTTCATTT	AGTTTGATTA	TTCAGTGTCA	CTGGCGACAC	GTAGCAGCTT	AGACTAAGGC	600
CATTATTGTA	CTTGCCTTAT	TAGAGTGTCT	TTCCACGGAG	CCACTCCTCT	GACTCAGGGC	660
TCCTGGGTTT	TGTATTCTCT	GAGCTGTGCA	GGTGGGGAGA	CTGGGCTGAG	GGAGCCTGGC	720
CCCATGGTCA	GCCCTAGGGT	GGAGAGGCCAC	CAAGAGGGAC	GCCTGGGGGT	GCCAGGACCA	780
GTCAACCTGG	GCAAAGCCTA	GTGAAGGCTT	CTCTCTGTGG	GATGGGATGG	TGGAGGGCCA	840
CATGGGAGGC	TCACCCCCCTT	CTCCATCCAC	ATGGGAGCCG	GGTCTGCCTC	TTCTGGGAGG	900
GCAGCAGGGC	TACCCTGAGC	TGAGGCAGCA	GTGTGAGGCC	AGGGCAGAGT	GAGACCCAGC	960
CCTCATCCCG	AGCACCTCCA	CATCCTCCAC	GTTCTGCTCA	TCATTCTCTG	TCTCATCCAT	1020
CATCATGTGT	GTCCACGACT	GTCTCCATGG	CCCCGAAAAA	GGACTCTCAG	GACCAAAGCT	1080
TTCATGTAAA	CTGTGCACCA	AGCAGGAAAT	GAAAATGTCT	TGTGTTACCT	GAAAACACTG	1140
TGCACATCTG	TGTCTTGTGT	GGAATATTGT	CCATTGTCCA	ATCCTATGTT	TTTGTTCAAA	1200
GCCAGCGTCC	TCCTCTGTGA	CCAATGTCTT	GATGCATGCA	CTGTTCCCCC	TGTGCAGCCG	1260
CTGAGCGAGG	AGATGCTCCT	TGGGCCCTT	GAGTGCAGTC	CTGATCAGAG	CCGTGGCCT	1320
TTGGGGTGAA	CTACCTTGGT	TCCCCCACTG	ATCACAAAAA	CATGGTGGGT	CCATGGCAG	1380
AGCCCAAGGG	AATTGGTGT	GCACCAGGGT	TGACCCCAGA	GGATTGCTGC	CCCATCAGTG	1440
CTCCCTCACA	TGTCAGTACC	TTCAAACTAG	GGCCAAGCCC	AGCACTGCTT	GAGGAAAACA	1500
AGCATTACACA	ACTTGTFFFF	GGTTTTAAA	ACCCAGTCCA	CAAATAACC	AATCCTGGAC	1560
ATGAAGATTC	TTTCCCAATT	CACATCTAAC	CTCATCTTCT	TCACCATTG	GCAATGCCAT	1620
CATCTCCTGC	CTTCCTCCTG	GGCCCTCTCT	GCTCTGCGTG	TCACCTGTGC	TTGGGCCCT	1680
TCCCCACAGGA	CATTCTCTA	AGAGAACAAAT	GTGCTATGTG	AAGAGTAAGT	CAACCTGCCT	1740
GACATTGGA	GTGTTCCCC	CCCACTGAGG	GCAGTCGATA	GAGCTGTATT	AAGCCACTTA	1800
AAATGTTCAC	TTTGACAAA	GGCAAGCACT	TGTGGGTTTT	TGTTTTGTTT	TTCATTCACT	1860
CTTACGAATA	CTTTGCCCT	TTGATTAAAG	ACTCCAGTTA	AAAAAAATT	TAATGAAGAA	1920
AGTGGAAAAC	AAGGAAGTCA	AAGCAAGGAA	ACTATGTAAC	ATGTAGGAAG	TAGGAAGTAA	1980
ATTATAGTGA	TGTAATCTTG	AATTGTAACT	GTTCGTGAAT	TTAATAATCT	GTAGGGTAAT	2040
TAGTAACATG	TGTTAAAGTAT	TTTCATAAGT	ATTTCAAATT	GGAGCTTCAT	GGCAGAAGGC	2100
AAACCCATCA	ACAAAAATTG	TCCCTTAAAC	AAAAATTAAA	ATCCTCAATC	CAGCTATGTT	2160
ATATTGAAAA	AATAGAGCCT	GAGGGATCTT	TACTAGTTAT	AAAGATACAG	AACTTTCA	2220

AAACCTTTG AAATTAACCT CTCACTATAC CAGTATAATT GAGTTTCAG TGGGGCAGTC	2280
ATTATCCAGG TAATCCAAGA TATTTAAAAA TCTGTCACGT AGAACTTGGA TGTACCTGCC	2340
CCCAATCCAT GAACCAAGAC CATTGAATTTC TTGGTTGAGG AAACAAACAT GACCCTAAAT	2400
CTTGACTACA GTCAGGAAAG GAATCATTTC TATTTCTCCT CCATGGGAGA AAATAGATAA	2460
GAGTAGAAC AC TGCAAGGAAA ATTATTTGCA TAACAATTCC TCTACTAAC A ATCAGCTCCT	2520
TCCTGGAGAC TGCCCAGCTA AAGCAATATG CATTAAATA CAGTCTTCCA TTTGCAAGGG	2580
AAAAGTCTCT TGTAATCCGA ATCTCTTTT GCTTCGAAC TGCTAGTCAA GTGCGTCCAC	2640
GAGCTGTTA CTAGGGATCC CTCATCTGTC CCTCCGGGAC CTGGTGCTGC CTCTACCTGA	2700
CACTCCCTTG GGCTCCCTGT AACCTCTTC GAGGCCCTCG CTGCCAGCTC TGTATCAGGA	2760
CCCAGAGGAA GGGGCCAGAG GCTCGTTGAC TGGCTGTGTG TTGGGATTGA GTCTGTGCCA	2820
CGTGTATGTG CTGTGGTGTG TCCCCCTCTG TCCAGGC ACT GAGATACCA CGAGGAGGCT	2880
CCAGAGGGCA CTCTGCTTGT TATTAGAGAT TACCTCCTGA GAAAAAAGCT TCCGCTTGG	2940
GCAGAGGGC TGAATAGCAG AAGGTTGCAC CTCCCCAAC CTTAGATGTT CTAAGTCTTT	3000
CCATTGGATC TCATTGGACC CTTCCATGGT GTGATCGTCT GACTGGTGTG ATCACCGTGG	3060
GCTCCCTGAC TGGGAGTTGA TCGCCTTCC CAGGTGCTAC ACCCTTTCC AGCTGGATGA	3120
GAATTGAGT GCTCTGATCC CTCTACAGAG CTTCCCTGAC TCATTCTGAA GGAGCCCCAT	3180
TCCTGGAAA TATTCCCTAG AAACCTCCAA ATCCCCTAAG CAGACCACTG ATAAAACCAT	3240
GTAGAAAATT TGTTATTTG CAACCTCGCT GGACTCTCAG TCTCTGAGCA GTGAATGATT	3300
CAGTGTAAA TGTGATGAAT ACTGTATTT GTATTGTTTC AAGTGCATCT CCCAGATAAT	3360
GTGAAAATGG TCCAGGAGAA GGCCAATTCC TATACGCAGC GTGCTTAAA AAATAAATAA	3420
GAAACAACTC TTTGAGAAC AACAAATTCT ACTTTGAAGT CATAACCAATG AAAAAATGTA	3480
TATGCACCTA TAATTTCT AATAAAGTTC TGTACTCAAA TGTAAA	3526

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Ala Lys Asp Val Lys His His His His His Gly Ser Gly Ser  
1 5 10 15

Asp Asp Asp Asp Lys  
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA construct"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAAACCAG TATCTCTGTC TTATCGTTGT CCATGCCGAT TCTTCGAAAG CCATGTTGCC	60
AGAGCCAACG TCAAGCATCT CAAAATTCTC AACACTCCAA ACTGTGCCCT TCAGATTGTA	120
GCCCGGCTGA AGAACAAACAA CAGACAAGTG TGCATTGACC CGAAGCTAAA GTGGATTTCAG	180
GAGTACCTGG AGAAAGCTTT AAACAAG	207

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA construct"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAACCAG TATCTCTGTC TTATCGTTGT CCATGCCGAT TCTTCGAAAG CCATGTTGCC	60
AGAGCCAACG TCAAGCATCT CAAAATTCTC AACACTCCAA ACTGTGCCCT TCAGATTGTA	120
GCCCGGCTGA AGAACAAACAA CAGACAAGTG TGCATTGACC CGAAGCTAAA GTGGATTTCAG	180

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 270 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA construct"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCAGCTA AAGACGTAAA ACATCACCAT CACCACG GTTCTGGTTC TGATGACGAT	60
GACAAAAAAC CAGTATCTCT GTCTTATCGT TGTCCATGCC GATTCTTCGA AAGCCATGTT	120
GCCAGAGCCA ACGTCAAGCA TCTCAAAATT CTCAACACTC CAAACTGTGC CCTTCAGATT	180
GTAGCCCGGC TGAAGAACAA CAACAGACAA GTGTGCATTG ACCCGAAGCT AAAGTGGATT	240
CAGGAGTACC TGGAGAAAGC TTTAAACAAG	270

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA construct"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGCAGCTA AAGACGTAAA ACATCACCAT CACCACG GTTCTGGTTC TGATGACGAT	60
GACAAAAAAC CAGTATCTCT GTCTTATCGT TGTCCATGCC GATTCTTCGA AAGCCATGTT	120
GCCAGAGCCA ACGTCAAGCA TCTCAAAATT CTCAACACTC CAAACTGTGC CCTTCAGATT	180
GTAGCCCGGC TGAAGAACAA CAACAGACAA GTGTGCATTG ACCCGAAGCT AAAGTGGATT	240
CAGGAGTACC TGGAGAAAGC TTTAAACAAG CGTTTCAAAA TG	282

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu
1					5				10						15
Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr
							20			25				30	
Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg
					35			40				45			
Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu
					50		55				60				
Lys	Ala	Leu	Asn	Lys											
					65										

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu
1					5				10						15
Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr
							20			25				30	
Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg
					35			40				45			
Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu
					50		55				60				

Lys Ala Leu Asn Lys Arg Phe Lys Met  
65 70

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Ala Lys Asp Val Lys His His His His His Gly Ser Gly  
1 5 10 15

Ser Asp Asp Asp Asp Lys Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro  
20 25 30

Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu  
35 40 45

Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu  
50 55 60

Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile  
65 70 75 80

Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ala Ala Lys Asp Val Lys His His His His His Gly Ser Gly  
1 5 10 15

Ser Asp Asp Asp Asp Lys Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro

20

25

30

Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu  
35 40 45

Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu  
50 55 60

Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile  
65 70 75 80

Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
85 90

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser  
1 5 10 15

His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro  
20 25 30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Arg Gln  
35 40 45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys  
50 55 60

Ala Leu Asn Lys  
65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser  
1                   5                   10                   15

His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro  
20                   25                   30

Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln  
35                   40                   45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys  
50                   55                   60

Ala Leu Asn Lys Arg Phe Lys Met  
65                   70